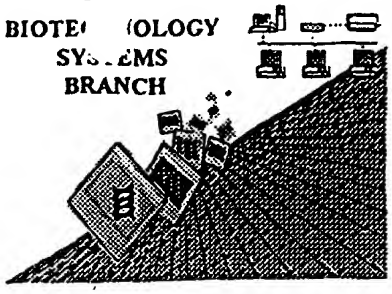
A. Kebede

#12

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/445,480

Source: OIPE

Date Processed by STIC: 9/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/445,480*

INPUT SET: S36623.raw

OIPE

Does Not Comply
Corrected Diskette Needed

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

Format: ← Surname comma OTHER NAMES.

(i) APPLICANT:
(A) NAME: DLO-Center for Plant Breeding and Reproduction Research
(B) ~~STREET: Droevendaalsesteeg 1~~
(C) ~~CITY: Wageningen~~
(E) ~~COUNTRY: The Netherlands~~
(F) ~~POSTAL CODE (ZIP): 6708~~ PB
(G) ~~TELEPHONE: +31 317 477001~~
(H) ~~TELEFAX: +31 317 418094~~
(I) ~~TELEX:~~ -

remove →

* See sample in Sequence Rules provided.

(ii) TITLE OF INVENTION: A method for plant protection against insects or nematodes

(iii) NUMBER OF SEQUENCES: 4

← insert (iv) CORRESPONDENCE ADDRESS

~~(iv)~~ (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

* see format in Sequence Rules provided.

(v) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/NL98/00352

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 888 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Actinia equina

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION:99..695

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:3..695

(ix) FEATURE:
(A) NAME/KEY: sig_peptide
(B) LOCATION:3..98

(ix) FEATURE:
(A) NAME/KEY: 5'UTR
(B) LOCATION:1..2

(ix) FEATURE:
(A) NAME/KEY: 3'UTR
(B) LOCATION:696..888

(x) PUBLICATION INFORMATION:
(A) AUTHORS: Gruden, Kristina
Strukelj, Borut
Popovic, Tatjana
Lenarcic, Brigita
Bevec, Tadeja
Brzin, Joze
Kregar, Igor
Herzog-Velikonja, Jana
Stiekema, Willem J
Bosch, Dirk
(B) TITLE: The cysteine protease activity of Colorado potato beetle (Leptinotarsa decemlineata) guts, which is insensitive to potato protease inhibitors, is inhibited by thyroglobulin type-1 domain inhibitors
(C) JOURNAL: Insect Biochem. Mol. Biol
(D) VOLUME: 28
(F) PAGES: 549-560
(G) DATE: 1998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
CT ATG GCT CTT AGC CAA AAC CAA GCC AAG TTT TCC AAA GGA TTC GTC          47
   Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val
   -32     -30                 -25                 -20

GTG ATG ATT TGG GTA CTA TTC ATT GCT TGT GCT ATA ACT TCA ACT GAA         95
Val Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu
        -15                 -10                  -5

GCT AGT CTA ACC AAA TGC CAA CAG CTC CAG GCC TCG GCT AAC AGT GGT        143
Ala Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly
```

```
100         1               5                  10                  15
101
102   CTG ATA GGT ACT TAT GTA CCA CAA TGC AAA GAA ACG GGA GAG TTC GAA       191
103   Leu Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu
104                   20                  25                  30
105
106   GAA AAA CAA TGC TGG GGA TCG ACT GGT TAC TGT TGG TGT GTG GAT GAA       239
107   Glu Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu
108               35                  40                  45
109
110   GAT GGA AAA GAG ATT CTA GGA ACC AAG ATC CGT GGA TCT CCG GAT TGC       287
111   Asp Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys
112            50                  55                  60
113
114   AGC CGC AGA AAA GCC GCG TTA ACA CTT TGC CAG ATG ATG CAA GCC ATC       335
115   Ser Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile
116        65                  70                  75
117
118   ATT GTT AAT GTC CCT GGT TGG TGT GGC CCT CCA TCG TGT AAA GCT GAC       383
119   Ile Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp
120    80                  85                  90                  95
121
122   GGC AGT TTT GAC GAG GTT CAG TGC TGC GCA AGT AAT GGA GAA TGC TAC       431
123   Gly Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr
124                 100                 105                 110
125
126   TGT GTG GAT AAG AAA GGA AAA GAA CTT GAA GGC ACA AGA CAA CAG GGA       479
127   Cys Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly
128             115                 120                 125
129
130   AGG CCA ACC TGC GAA AGA CAC CTA AGC GAA TGC GAG GAA GCT CGA ATC       527
131   Arg Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Glu Ala Arg Ile
132           130                 135                 140
133
134   AAG GCG CAT TCA AAC AGT CTT CGT GTT GAG ATG TTC GTG CCA GAG TGT       575
135   Lys Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys
136       145                 150                 155
137
138   TTA GAA GAT GGA TCA TAT AAC CCA GTA CAG TGC TGG CCT AGC ACA GGA       623
139   Leu Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly
140   160                 165                 170                 175
141
142   TAC TGT TGG TGC GTC GAT GAA GGA GGG GTA AAG GTA CCA GGT TCC GAT       671
143   Tyr Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp
144                 180                 185                 190
145
146   GTC AGA TTT AAA CGC CCC ACA TGC TAAGAAAAAC ACAGTGAACA AAGTGGCTAG       725
147   Val Arg Phe Lys Arg Pro Thr Cys
148             195
149
150   TTTCCAGATC GAAAATAACT ACAAAGGATT AATAAAATGT TAAAATAATT TCTCAATTCG      785
151
152   GCTGTGATAT ATTTTTTCCA AGATAATTTA ATCTGCATGT AGTTAACAGA AAACAATCTC      845
```

AACTAGAAAT AAAGACTACG GTAATAATGA CAAAAAAAAA AAA 888

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 231 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val Val
-32  -30                 -25                 -20

Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu Ala
-15                 -10                  -5

Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly Leu
  1               5                  10                  15

Ile Gly Thr Tyr Val Pro Gln Cys Lys Glu Thr Gly Glu Phe Glu Glu
             20                  25                  30

Lys Gln Cys Trp Gly Ser Thr Gly Tyr Cys Trp Cys Val Asp Glu Asp
          35                  40                  45

Gly Lys Glu Ile Leu Gly Thr Lys Ile Arg Gly Ser Pro Asp Cys Ser
      50                  55                  60

Arg Arg Lys Ala Ala Leu Thr Leu Cys Gln Met Met Gln Ala Ile Ile
 65                  70                  75                  80

Val Asn Val Pro Gly Trp Cys Gly Pro Pro Ser Cys Lys Ala Asp Gly
                 85                  90                  95

Ser Phe Asp Glu Val Gln Cys Cys Ala Ser Asn Gly Glu Cys Tyr Cys
            100                 105                 110

Val Asp Lys Lys Gly Lys Glu Leu Glu Gly Thr Arg Gln Gln Gly Arg
        115                 120                 125

Pro Thr Cys Glu Arg His Leu Ser Glu Cys Glu Glu Ala Arg Ile Lys
    130                 135                 140

Ala His Ser Asn Ser Leu Arg Val Glu Met Phe Val Pro Glu Cys Leu
145                 150                 155                 160

Glu Asp Gly Ser Tyr Asn Pro Val Gln Cys Trp Pro Ser Thr Gly Tyr
                165                 170                 175
```

```
Cys Trp Cys Val Asp Glu Gly Gly Val Lys Val Pro Gly Ser Asp Val
            180                 185                 190

Arg Phe Lys Arg Pro Thr Cys
        195

(2) INFORMATION FOR SEQ ID NO: 3:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 696 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

   (iii) HYPOTHETICAL: NO

    (iv) ANTI-SENSE: NO

     (vi) ORIGINAL SOURCE:
          (A) ORGANISM: Actinia equina

    (vii) IMMEDIATE SOURCE:
          (B) CLONE: optimized gene for expression in plants

     (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION:1..693

     (ix) FEATURE:
          (A) NAME/KEY: mat_peptide
          (B) LOCATION:97..693

     (ix) FEATURE:
          (A) NAME/KEY: sig_peptide
          (B) LOCATION:1..693

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ATG GCT CTT AGC CAG AAC CAG GCC AAG TTT TCC AAG GGA TTC GTC GTG      48
Met Ala Leu Ser Gln Asn Gln Ala Lys Phe Ser Lys Gly Phe Val Val
-32     -30                 -25                 -20

ATG ATT TGG GTA CTA TTC ATT GCT TGT GCT ATC ACT TCA ACT GAA GCT      96
Met Ile Trp Val Leu Phe Ile Ala Cys Ala Ile Thr Ser Thr Glu Ala
    -15                 -10                  -5

AGT CTA ACG AAA TGC CAA CAG CTG CAG GCC TCG GCT AAC AGT GGT CTG     144
Ser Leu Thr Lys Cys Gln Gln Leu Gln Ala Ser Ala Asn Ser Gly Leu
  1               5                  10                  15
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/445,480*

DATE: 09/25/2001
TIME: 04:28:46

INPUT SET: S36623.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: DLO-Center for Plant Breeding and
8	Unknown or Misplaced Identifier	(B) STREET: Droevendaalsesteeg 1
9	Unknown or Misplaced Identifier	(C) CITY: Wageningen
10	Unknown or Misplaced Identifier	(E) COUNTRY: The Netherlands
11	Unknown or Misplaced Identifier	(F) POSTAL CODE (ZIP): 6708 PB
12	Unknown or Misplaced Identifier	(G) TELEPHONE: +31 317 477001
13	Unknown or Misplaced Identifier	(H) TELEFAX: +31 317 418094
14	Unknown or Misplaced Identifier	(I) TELEX: -

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/09/445,480*

DATE: 09/25/2001
TIME: 04:28:46

INPUT SET: S36623.raw

ADDRESSEE
STREET
CITY
STATE
COUNTRY
ZIP
CORRESPONDENCE ADDRESS
APPLICATION NUMBER
FILING DATE
CLASSIFICATION
APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

SEQUENCE CORRECTION REPORT
PATENT APPLICATION *US/09/445,480*

DATE: 09/25/2001
TIME: 04:28:46

INPUT SET: S36623.raw

Line	Original Text	Corrected Text